

GAP of: 0964sid2 check: 7022 from: 1 to: 405

WPDEF Case 0964 Rad23 SEQ ID NO: 2 corn
Case 0964 Rad23 SEQ ID NO: 2 corn

to: 0964DY12013aa check: 506 from: 1 to: 382

WPDEF Case 0964D Rad23 protein encoded by GenBank Y12013 carrot
Case 0964D Rad23 protein encoded by GenBank Y12013 carrot
Y12013. *Daucus carota* mRNA. . .[gi:1914682] Links
LOCUS DCRAD23I 1496 bp mRNA linear PLN 28-JAN-1999
DEFINITION *Daucus carota* mRNA for RAD23 protein, isoform I.
ACCESSION Y12013 . . .

Symbol comparison table: /app/gcg/10.2/gcgcore/data/rundata/blosum62.cmp
CompCheck: 1102

BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. *Proc. Natl. Acad.
Sci. USA* 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Quality:	1169	Length:	407
Ratio:	3.060	Gaps:	8
Percent Similarity:	71.053	Percent Identity:	65.789

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

0964sid2 x 0964DY12013aa March 31, 2003 14:17 ..

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      .
1 MKLNVKTLKGTNFEIEASPDASVADV KRIIETTQGGSTYRADQQMLIYQG 50
  ||: |||||. |||: .|| ||||| ||| || . | | |||||
1 MKIYVKTLKGSQFEIQVNPDDSVADV KRSIETAQGAAYPAAQQMLIYQG 50
      .
51 KILKDETTLESNGVAENSFLVIMLSKAKASSSGASTATTAKAPATLAQPA 100
  |: ||| ||| | |||||: |||||. |. | || .|| || |
51 KVLKDGTTLLENNVAENSFIVIMLSKSKSPSGEGSTTSTAAAPKAPQTS 100
      .
101 APVAPAASVARTPTQA.PVATAETAPPSVQPQAAPAAATVAATDDADV 149
  | || .|. | || || || | || . | :|. ||
101 PPSVPAPAVSQPPASTLPVPAPSPAP...APATAPIPSAAVGSEANV 147
      .
150 AASNLVFGNNLEQTIQQIILDMGGGTWERDTVVRALRAAYNNPERAIDY 199
  ||| || |. ||| |||||: ||||: | .||: |||||: |||
148 AASLLVAGSNLEGAIQQIILDMGGGTWDRDTVIRIVRAAFNNPERAVE 197
      .
200 SGIPENVEAQPVARAPAAGQQTNQQAASPA.QPAVALPVQPSPASAGP 248
  ||||| || ||| .| .| |||. | || | ||. |||||
198 SGIPEQAEAPPVAPSPPSG.....QAANPLDQPPAA..AQPA PAS 240
      .

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249 NPLNLFPGVPSGGSNPGVVPGAGSGALDALRQLPQFQALLQLVQANPQI 298
 |||.|||||.| ||| ||.| || || ||||| :||.||||
 241 NPLDLFPQGLPDMGSN.....AAGAGNLDFLRTNQQFQALRAMVQSNPQI 285
 299 LQPMLQELGKQNPQILRLIQENQAEFLRLVNESPEGGPGGNILGQLAAAV 348
 ||||| ||||| :||| ||.||:||.||:|| ||| |:||
 286 LQPMLQELGKQNPFLMRLIQEHQADFLQLINEPMEGGE..NLLGH....G 329
 349 PQTLTVTPEEREAIQRLEGMGFNRELVLEVFFACNKDEELTANYLLDHGH 398
 || :.|||||:||:|||| |||.||||| |||||.||| ||||| |
 330 PQAISVTPEERDAIERLEAMGFDRELVLEVFFACNKNEELAANYLLDHMH 379
 399 EFDDQQQ 405
 ||:
 380 EFE.... 382